

Figure 1

2020-06-25-00

## Stability Study of SAHH

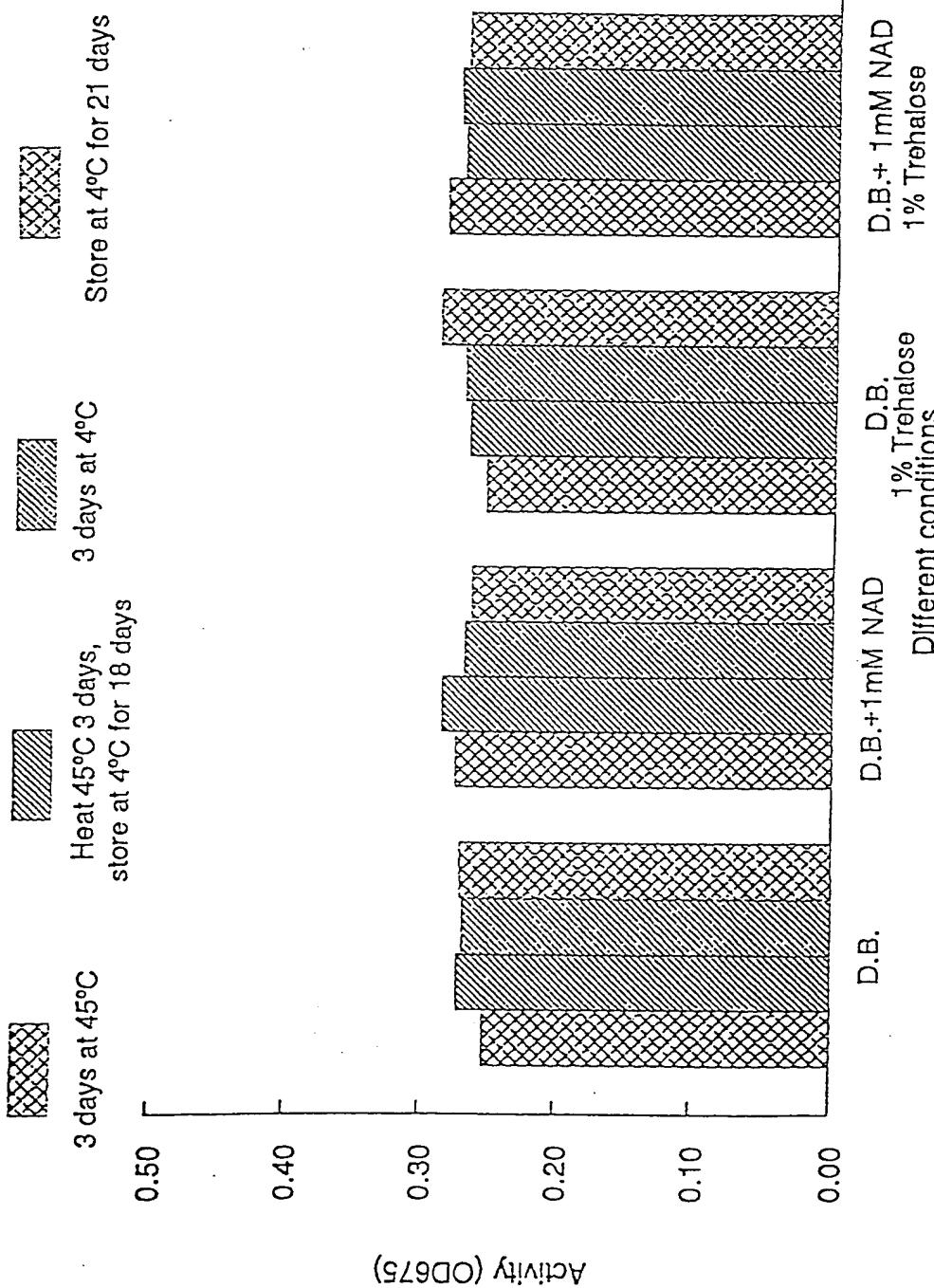


Figure 2

Title: HIGH EXPRESSION AND PRODUCTION OF HIGH-SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYL HOMOCYSTEINASE (SAHH) AND IMPROVED ASSAY FOR S-ADENOSYLMETHIONINE (SAM)  
First Inventor: Robert M. HORN, et al.  
Application No.: 09/759,990  
Docket No.: 31276-20026.00  
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# Screening of SAHH

Title: HIGH EXPRESSION AND PRODUCTION OF HIGH-SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYL HOMOCYSTEINASE (SAHH) AND IMPROVED ASSAY FOR S-ADENOSYLMETHIONINE (SAM)  
First Inventor: Robert M. ROSENSTEIN, et al.  
Application No.: 09/759,990  
Docket No.: 31276-20026.00  
Sheet 3 of 8

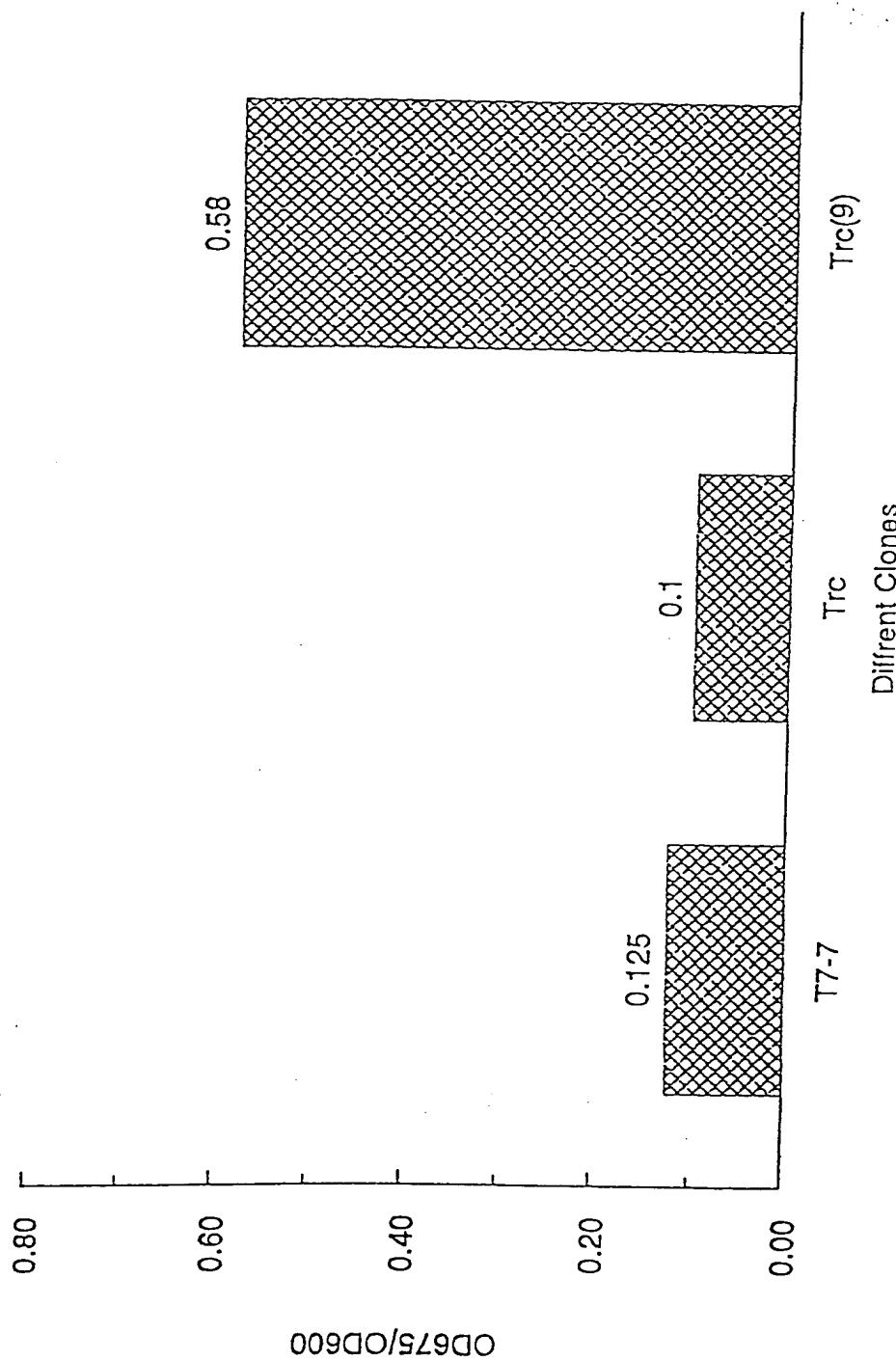


Figure 3

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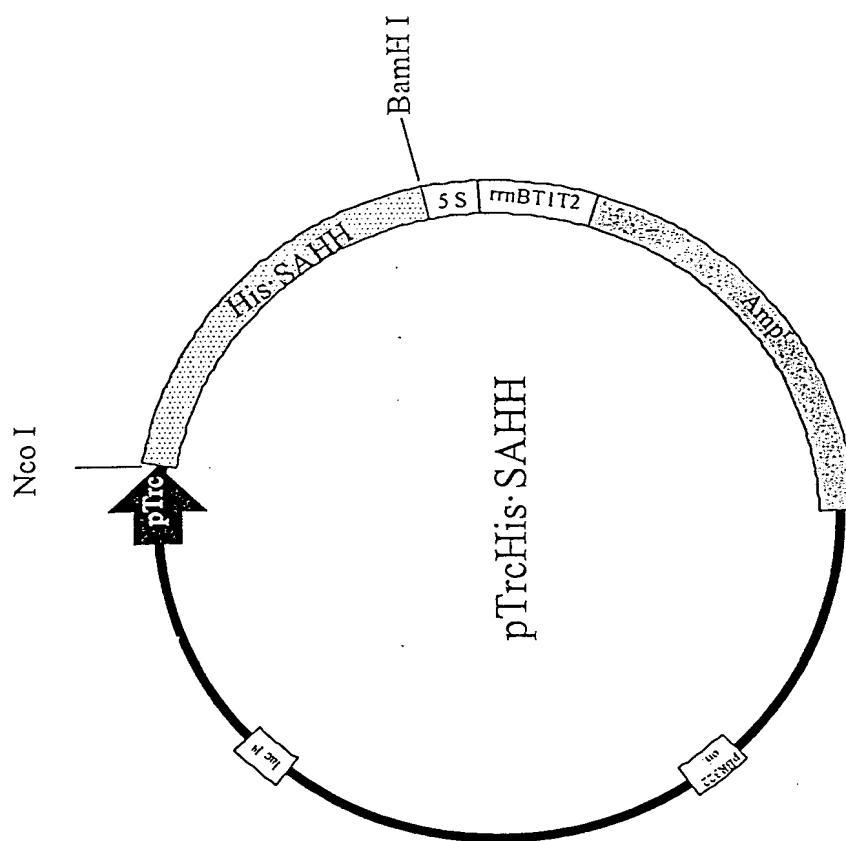


Figure 4

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Stability of SAHH.His

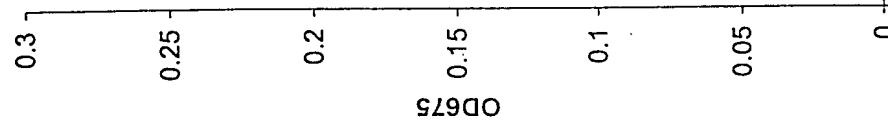


Figure 5

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

SAHH-wild	291	ATGGCTTGCAAATCACCTGCTGGTGTCCATTGAGTACAGAATTGCCGACATCAACCTC
A/C,	71	ATGGCTTGCAAATCACCTACTGGTGTCCATTGAGTACAGAATTGCCGACATCAACCTC
*****		
SAHH-wild	351	CATGTTCTCGGCCGTAAAGGAACCTACCCCTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,	131	CATGTTCTCGGCCGTAAAGGAACCTACCCCTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
*****		
SAHH-wild	411	CTTCGTGAGCGTTATTCCGCTTCTAACGCCATTGAAGGGTGTCAAGAATCTCTGGTCCCTC
A/C,	191	CTTCGTGAGCGTTATTCCGCTTCTAACGCCATTGAAGGGTGTCAAGAATCTCTGGTCCCTC
*****		
SAHH-wild	471	CACATGACAGTCCAGACAGCGGTCTTATTGAGACACTCACAGCTTGGTGTGATGTC
A/C,	251	CACATGACAGTCCAGACAGCGGTCTCATCGAGACACTCACAGCTTGGTGTGATGTC
*****		
SAHH-wild	531	AGATGGGCTCCTGCAACATCTCTACACAAGATAACAGCCGTGCTGCTATCGTTGTC
A/C,	311	AGATGGGCTCCTGCAACATCTCTACACAAGATAACAGCCGTGCTGCTATCGTTGTC
*****		
SAHH-wild	591	GGCCAACAGGCACACCAAGAGAACGCCAGCGGTATCCAGTCTTCGCTGGAGGGCGAA
A/C,	371	GGCCAACAGGCACACCAAGAGAACGCCAGCGGTATCCAGTCTTCGCTGGAGGGCGAA
*****		
SAHH-wild	651	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGCCAGATGGTCAAGGC
A/C,	431	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGCCAGATGGTCAAGGC
*****		
SAHH-wild	711	CCACAGCAGGTTGTCGATGATGGTGGTGTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,	491	CCACAGCAGGTTGTCGATGATGGTGGTGTACACTCCTCATCTCCAAGGGCTTCGAA
*****		
SAHH-wild	771	TTCGAAACAGCGGTGCTGTCCTCCAGAGCCAACAGAACGCTGACAACTCGAATACCGCTGC
A/C,	551	TTCGAAACAGCGGTGCTGTCCTCCAGAGCCAACAGAACGCTGACAACTCGAATACCGCTGC
*****		
SAHH-wild	831	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGAACAAACCACAGTGGCACACAGTTGCT
A/C,	611	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGAACAAACCACAGTGGCACACAGTTGCT
*****		
SAHH-wild	891	GCCGGCATGAACGGTTCCGAAGAGAACACAACAGGTGTCCACCGCCTTACCGCTC
A/C,	671	GCCGGCATGAACGGTTCCGAAGAGAACACAACAGGTGTCCACCGCCTTACCGCTC
*****		
SAHH-wild	951	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,	731	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
*****		
SAHH-wild	1011	AAGTCGATAACATCTACGGCTGCGCACTCCATTACGATGGTATCAACCGTCTTCC
A/C,	791	AAGTCGATAACATCTACGGCTGCGCACTCCATTACGATGGTATCAACCGTCTTCC
*****		
SAHH-wild	1071	GATGTCATGATCGCGCAAGACAGCTCTCGTCATGGTTACGGCATGTCGGAGGGC
A/C,	851	GATGTCATGATCGCGCAAGACAGCTCTCGTCATGGTTACGGCATGTCGGAGGGC
*****		
SAHH-wild	1131	TCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCTTATCATCACAGAAGTCGACCCATC
A/C,	911	TCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCTTATCATCACAGAAGTCGACCCATC
*****		

Figure 6a

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SAHH-wild	1191	TGCGCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
A/C,	971	TGCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
*****		
SAHH-wild	1251	GATGTCGATATCTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
A/C,	1031	GATGTCGATATCTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
*****		
SAHH-wild	1311	GCCCAGATGAAGGATAAGGCTATTGTCGGAACATCGGCCACTTCGATAACGAAATTGAT
A/C,	1091	GCCCAGATGAAGGATAAGGCTATTGTCGGAACATCGGCCACTTCGATAACGAAATTGAT
*****		
SAHH-wild	1371	ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCAAATCAAGCCAGAACATGAC
A/C,	1151	ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCAAATCAAGCCAGAACATGAC
*****		
SAHH-wild	1431	ATGTGGGAATTCCCAGATGGCACGCTATCCTCCTTCTTGTGCTGAGGGCCGCCTTCTTAAC
A/C,	1211	ATGTGGGAATTCCCAGATGGCACGCTATCCTCCTTCTTGTGCTGAGGGCCGCCTTCTTAAC
*****		
SAHH-wild	1491	CTTGGTTGCGCTACAGGTACCCATTTGTTATGCAATGTCATTCAAAACCAAGACA
A/C,	1271	CTTGGCTGCGCTACAGGTACCCATTTGTTATGCAATGTCATTCAAAACCAAGACA
*****		
SAHH-wild	1551	CTCGCTCAGCTGACCTCTACGAAAAGAGAGGAAATCTGAGATGAAGGTTACACACTT
A/C,	1331	CTCGCTCAGCTGACCTCTACGAAAAGAGAGGAAATCTGAGAAGAAGGTTACACACTT
*****		
SAHH-wild	1611	CCGAAGCATCTCGATGAAAGAAGTCGTTGCCACCTCGGATCTCGATGTCACACCTT
A/C,	1391	CCGAAGCATCTCGATGAAAGAAGTCGCTGCCACCTCGGATCTCGATGTCACACCTT
*****		
SAHH-wild	1671	ACAAAGCTTACACAGAACAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG
A/C,	1451	ACAAAGCTTACACAGAACAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG
*****		
SAHH-wild	1731	TCTGATGCTTACCGTTATTAA
A/C,	1511	TCTGATGCTTACCGTTATTAA
*****		

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65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

SAHH-wild	782	CGGTGCTGTCCCAGAGCCAACAGAACAGCTGACAACCTCGAACATACC
A/C,	682	CGGTGTTCCGAAGAGACAACAACAGGTGTCACCGCCCTCTACC
*****		

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80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild	1053	GGTATCAACCGTGCTTCCGA
A/C,	674	GGCATGAACGGTGTTCGCA
*****		

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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 564 GATAACAGCCGCTGCTG  
A/C, 554 GAAACAGCCGGTGCTG  
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64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1224 GTCCGCCGATCGAGGAAGTCGTCAAGGATGTCGATATCTTC  
A/C, 710 GTCCACCGCCCTCTACCAGCTCGAGAAGGAGGGCAAACCTCTC  
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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 774 GAAACAGCCGGTGCTG  
A/C, 344 GATAACAGCCGCTGCTG  
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